



RA	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D., Merklikov G., Milshina N.V., Mobray C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzy D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nuskein D.R., Pacieb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Renert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Sjoden-Kamors I., Simpson M., Skupski M.P., Smith T., Spier E., Spreading C., Stapleton M., Strong R., Sun E., Svärskas R., Tector C., Turner E., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhang M., Zhang G., Zhao O., Zheng L., Zheng X.H., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;	Db	241 YNMKDURRLEVQDASKPLGLAGHKDKRMACMFVAGVDPNGALGSVDIKPQDEIVEV 300
RA	"The genome of <i>Drosophila melanogaster</i> .";	Qy	301 NGNVLKRNCHLNASAVFKNDGDKLMLTISRRKPNDEGMCKPKPFTASDETRKFIDQ 360
RA	Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.	Db	301 NGNVLKRNCHLNASAVFKNDGDKLMLTISRRKPNDEGMCKPKPFTASDETRKFIDQ 360
RA	SEQUENCE FROM N.A.	Qy	361 FPKARTVQVRREGFLGIMVYKGKREVGSCFISFDLREGSNSAELAGVKYGDMLAVNODV 420
RC	TISSUE=COMPOUND EYE;	Db	361 FPKARTVQVRREGFLGIMVYKGKREVGSGIFISDLREGSNSAELAGVKYGDMLAVNODV 420
RL	Lindley D.L., Zinn G.G.; "The genome of <i>Drosophila melanogaster</i> .";	Qy	421 TLESNYDDATGLLRKAEGVYTMILITLKSEBAIAKEAKAEKKKEEAKKEEAKPEATA 480
RN	Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.	Db	421 TLESNYDDATGLLRKAEGVYTMILITLKSEBAIAKEAKAEKKKEEAKKEEAKPEATA 480
[3]	SEQUENCE FROM N.A.	Qy	481 EIKPNKKIILTEKPKMCHRQRQKOPCHDWL---NHPRLS-----GGQVA 528
RC	TISSUE=COMPOUND EYE;	Db	481 EIKPNKKIILTEKPKMCHRQRQKOPCHDWL---NHPRLS-----GGQVA 528
RX	MEDLINE-9512229; Published=7826638;	Qy	529 DKRKIFDHICDINGTPIHGSMTTLKVHQLFHHTYEAKVLTFRADPELEMFDLM 588
RA	Shieh B.H., Niemeyer B.;	Db	529 DKRKIFDHICDINGTPIHGSMTTLKVHQLFHHTYEAKVLTFRADPELEMFDLM 588
RT	"A novel protein encoded by the Inad gene regulates recovery of visual transduction in <i>Drosophila</i> .";	Qy	589 KKAKKELGLSLSPNBIGCTADLQGQYBEIDLQSRGSDITKNGDALEGFLPFCVAL 648
RL	Neuron 14:201-210(1995).	Db	589 KKAKKELGLSLSPNBIGCTADLQGQYBEIDLQSRGSDITKNGDALEGFLPFCVAL 648
RN	[4]	Db	649 FGKANGKVSMEVTRPKPTLREAPKA 674
RP	SEQUENCE FROM N.A.	Qy	649 FGKANGKVSMEVTRPKPTLREAPKA 674
RC	TISSUE=COMPOUND EYE;	Db	649 FGKANGKVSMEVTRPKPTLREAPKA 674
RA	Shieh B.;	Qy	590 Q9N8V3 PRELIMINARY; PRT: 674 AA.
RL	Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.	AC	Q9N8V3;
RP	[5]	DT	01-OCT-2000 (Tremblrel. 15, Last sequence update)
RC	SEQUENCE FROM N.A.	DT	01-DEC-2001 (Tremblrel. 19, Last annotation update)
RA	Tissue: Eye;	DE	INAD.
RL	Submitted (SRP-1998) to the EMBL/GenBank/DBJ databases.	GN	CG3504.
DR	EMBL: AE003458; AAC46915.1; -.	OS	<i>Drosophila melanogaster</i> (Fruit fly).
DR	EMBL: UI5803; ARG36490.1; -.	OC	Pterygota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; OC
DR	HSPP; P31016; IBPE.	OC	Ephydriidae; Drosophilidae; Drosophila.
DR	FlyBase; FBgn0001263; inad.	OX	NCBI_TAXID:7227.
DR	InterPro; IPR001478; PDZ.	RN	[1]
PR	SMART; SM00228; PDZ; 5.	RP	SEQUENCE FROM N.A.
DR	PROSITE; PS50106; PDZ; 5.	RC	STRAIN=CANTON-S.
SQ	SEQUENCE 674 AA; 74302 MW; D4C24091D99EE73 CRC64;	RA	Asari M., Shieh B.;
Query Match	95.0%; Score 3317; DB 5; Length 674;	RT	"The Inad locus in <i>Drosophila</i> ."
Best Local Similarity	95.3%; Pred. No. 2, 5e-200;	RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
Matches	654; Conservative 1; Mismatches 7; Indels 24; Gaps 3;	DR	EMBL: AF245280; AAC81203.1; -.
OY	1 MYQFLGKQGTAGELIHAVTLDKTGKSFVICRGEVKDSPNTKTGFIFGIVPDSPAH 60	DR	HSPP; P31016; IBPE.
Db		DR	FlyBase; FBgn0001263; inad.
OY	1 MYQFLGKQGTAGELIHAVTLDKTGKSFVICRGEVKDSPNTKTGFIFGIVPDSPAH 60	DR	InterPro; IPR001478; PDZ.
Db		DR	SMART; SM00228; PDZ; 5.
OY	61 LGGRLYKGDRILSNGKDVRSQEAVDILIKEADKIELEQTFDKSDEQAKSPRSN 120	DR	PROSITE; PS50106; PDZ; 5.
Db		DR	SEQUENCE 674 AA; 74305 MW; 55B1C57B7A100F1D CRC64;
OY	61 LGGRLYKGDRILSNGKDVRSQEAVDILIKEADKIELEQTFDKSDEQAKSPRSN 120	DR	Query Match 94.9%; Score 3312; DB 5; Length 574;
Db		DR	Best Local Similarity 95.2%; Pred. No. 5, 1e-200;
OY	121 GYMOAKNKFNEQOTINNAASGGQMGQOGQGQGMAGMMRQSMQKRNTFTASMRQKS 180	DR	Matches 653; Conservative 2; Mismatches 7; Indels 24; Gaps 3;
Db		DR	SEQUENCE 674 AA; 74305 MW; 55B1C57B7A100F1D CRC64;
OY	181 NYADEDEDDETRDMTRGIRTEAYEDRASAGCKLINKQEKORDKQEDFGYMAINKR 240	DR	Query Match 95.2%; Score 3312; DB 5; Length 574;
Db		DR	Best Local Similarity 95.2%; Pred. No. 5, 1e-200;
OY	181 NYADEDEDDETRDMTRGIRTEAYEDRASAGCKLINKQEKORDKQEDFGYMAINKR 240	DR	Matches 653; Conservative 2; Mismatches 7; Indels 24; Gaps 3;
OY	241 YNMKDLRREVDRASKPLGLAGHKDKRMACMFVAGVDPNGALGSVDIKPQDEIVEV 300	DR	SEQUENCE 674 AA; 74305 MW; 55B1C57B7A100F1D CRC64;
OY		DR	Query Match 95.2%; Score 3312; DB 5; Length 574;
Db	1 MYQFLGKQGTAGELIHAVTLDKTGKSFVICRGEVKDSPNTKTGFIFGIVPDSPAH 60	DR	Best Local Similarity 95.2%; Pred. No. 5, 1e-200;
OY	61 LGGRLYKGDRILSNGKDVRSQEAVDILIKEADKIELEQTFDKSDEQAKSPRSN 120	DR	Matches 653; Conservative 2; Mismatches 7; Indels 24; Gaps 3;
OY	61 LGGRLYKGDRILSNGKDVRSQEAVDILIKEADKIELEQTFDKSDEQAKSPRSN 120	DR	SEQUENCE 674 AA; 74305 MW; 55B1C57B7A100F1D CRC64;
OY	121 GYMOAKNKFNEQOTINNAASGGQMGQOGQGQGMAGMMRQSMQKRNTFTASMRQKS 180	DR	Query Match 95.2%; Score 3312; DB 5; Length 574;
Db		DR	Best Local Similarity 95.2%; Pred. No. 5, 1e-200;
OY	121 GYMOAKNKFNEQOTINNAASGGQMGQOGQGQGMAGMMRQSMQKRNTFTASMRQKS 180	DR	Matches 653; Conservative 2; Mismatches 7; Indels 24; Gaps 3;
OY	1 MYQFLGKQGTAGELIHAVTLDKTGKSFVICRGEVKDSPNTKTGFIFGIVPDSPAH 60	DR	SEQUENCE 674 AA; 74305 MW; 55B1C57B7A100F1D CRC64;
Db		DR	Query Match 95.2%; Score 3312; DB 5; Length 574;
OY	61 LGGRLYKGDRILSNGKDVRSQEAVDILIKEADKIELEQTFDKSDEQAKSPRSN 120	DR	Best Local Similarity 95.2%; Pred. No. 5, 1e-200;
OY	61 LGGRLYKGDRILSNGKDVRSQEAVDILIKEADKIELEQTFDKSDEQAKSPRSN 120	DR	Matches 653; Conservative 2; Mismatches 7; Indels 24; Gaps 3;
OY	121 GYMOAKNKFNEQOTINNAASGGQMGQOGQGQGMAGMMRQSMQKRNTFTASMRQKS 180	DR	SEQUENCE 674 AA; 74305 MW; 55B1C57B7A100F1D CRC64;
OY		DR	Query Match 95.2%; Score 3312; DB 5; Length 574;
Db	1 MYQFLGKQGTAGELIHAVTLDKTGKSFVICRGEVKDSPNTKTGFIFGIVPDSPAH 60	DR	Best Local Similarity 95.2%; Pred. No. 5, 1e-200;
OY	61 LGGRLYKGDRILSNGKDVRSQEAVDILIKEADKIELEQTFDKSDEQAKSPRSN 120	DR	Matches 653; Conservative 2; Mismatches 7; Indels 24; Gaps 3;
OY	121 GYMOAKNKFNEQOTINNAASGGQMGQOGQGQGMAGMMRQSMQKRNTFTASMRQKS 180	DR	SEQUENCE 674 AA; 74305 MW; 55B1C57B7A100F1D CRC64;
OY		DR	Query Match 95.2%; Score 3312; DB 5; Length 574;
Db	1 MYQFLGKQGTAGELIHAVTLDKTGKSFVICRGEVKDSPNTKTGFIFGIVPDSPAH 60	DR	Best Local Similarity 95.2%; Pred. No. 5, 1e-200;
OY	61 LGGRLYKGDRILSNGKDVRSQEAVDILIKEADKIELEQTFDKSDEQAKSPRSN 120	DR	Matches 653; Conservative 2; Mismatches 7; Indels 24; Gaps 3;
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OY		DR	Query Match 95.2%; Score 3312; DB 5; Length 574;
Db	1 MYQFLGKQGTAGELIHAVTLDKTGKSFVICRGEVKDSPNTKTGFIFGIVPDSPAH 60	DR	Best Local Similarity 95.2%; Pred. No. 5, 1e-200;
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OY	121 GYMOAKNKFNEQOTINNAASGGQMGQOGQGQGMAGMMRQSMQKRNTFTASMRQKS 180	DR	SEQUENCE 674 AA; 74305 MW; 55B1C57B7A100F1D CRC64;
OY		DR	Query Match 95.2%; Score 3312; DB 5; Length 574;
Db	1 MYQFLGKQGTAGELIHAVTLDKTGKSFVICRGEVKDSPNTKTGFIFGIVPDSPAH 60	DR	Best Local Similarity 95.2%; Pred. No. 5, 1e-200;
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OY		DR	Query Match 95.2%; Score 3312; DB 5; Length 574;

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## OM protein - protein search, using sw model

Run on:

May 8, 2003, 14:57:17 ; Search time 40 Seconds

(without alignments)

2245.273 Million cell updates/sec

Title: US-09-462-517-1

Perfect score: 3490

Sequence: 1 MVQFLGKQGTAGELIHMVTL..... KVSMEVTRPKPLTEAPKA 674

Scoring table: BIOSUMG2

Gapop 10.0 , Gapext 0.5

Searched:

908470 seqs., 133250620 residues

Total number of hits satisfying chosen parameters:

908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximal Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_11003:\*

/SIDS2/gcgdata/geneseq/geneseq/geneseq-emb1/AA1980.DAT:\*

2: /SIDS2/gcgdata/geneseq/geneseq/geneseq-emb1/AA1981.DAT:\*

3: /SIDS2/gcgdata/geneseq/geneseq/geneseq-emb1/AA1982.DAT:\*

4: /SIDS2/gcgdata/geneseq/geneseq/geneseq-emb1/AA1983.DAT:\*

5: /SIDS2/gcgdata/geneseq/geneseq/geneseq-emb1/AA1984.DAT:\*

6: /SIDS2/gcgdata/geneseq/geneseq/geneseq-emb1/AA1985.DAT:\*

7: /SIDS2/gcgdata/geneseq/geneseq/geneseq-emb1/AA1986.DAT:\*

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23: /SIDS2/gcgdata/geneseq/geneseq/geneseq-emb1/AA2002.DAT:\*

RESULT 1

RAW92953

ID AAW92953 standard; Protein; 674 AA.

XX AAW92953;

AC AAW92953;

XX DT 14-MAY-1999 (first entry)

XX DE Fly transducisome InaD protein.

XX KW InaD; transducisome; fly; insect; signal transduction protein; mutant; KW disorder.

XX OS Insecta.

XX FH Key Misc-difference 319

## ALIGNMENTS

Result No.	Score	Query Match Length	DB ID	Description
1	3490	100.0	674 20 AAW2953	Fly transducisome Dirosophila melanog Human PDZ1 protein
2	3317	95.0	674 22 ABP59957	Amino Acid Sequence
3	519	15.4	111 23 AABT7918	Protein containing Neuron-associated
4	537	15.4	2071 AAV353753	Protein containing Protein containing
5	533.5	15.3	2070 AAV04733	Mature Protein containing
6	523.5	15.0	856 21 AAB01383	Amino acid sequence
7	508	14.6	1373 20 AAV04730	
8	508	14.6	2000 20 AAV04732	
9	505.5	100.5	AAV04731	
10	491	14.5	1881 20 AAV24025	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

\* Description

Key Misc-difference 319

Location/Qualifiers

Misc-difference 501

/note= "Encoded by GT"

Misc-difference 508

/note= "Encoded by GAA"

Misc-difference 524

/note= "Encoded by GCA"

W0903974-A1.

XX PD 28-JAN-1999.

XX PF 15-JUL-1998;

XX PR 15-JUL-1998; 97US-0052588.

11	450	13.2	1627 22 ABG06117	Novel; human diagno PD2 domain-contain
12	446.5	12.8	763 20 AAY04741	Human protein SEQ
13	419	12.0	1552 22 AAM8793	Novel; human diagno
14	419	12.0	1554 22 ABO7288	Novel; human diagno
15	411	11.8	1584 22 ABO7290	Novel; human diagno
16	384	11.0	1526 22 ABG06116	Human PPML phosph
17	384	11.0	1526 22 AAM9777	Human prostate tum
18	241.5	6.9	2485 21 AAB19343	Novel; human diagno
19	241.5	6.8	2466 16 AAR71498	Amino acid sequenc
20	206.5	5.9	2466 19 AAW5999	Human protein tyro
21	238.5	6.8	2466 21 AAY0272	Intracellular prot
22	238.5	6.8	2466 20 AAY74151	Human PPML phosph
23	220	6.5	220 20 AAY4150	Human prostate tum
24	209.5	6.3	1239 20 AAY04734	Protein containing
25	206.5	5.9	354 23 ABB04799	Human PDZ3 prote
26	196.5	5.7	724 23 ABB04798	Drosophila melanog
27	201.5	5.8	871 22 ABB57855	Drosophila melanog
28	201.5	5.8	871 22 ABB67265	Human post-synapti
29	200.5	5.7	928 23 AAE21718	Protein DIg4 diffe
30	200.5	5.7	1037 22 ABB2366	Human protein cont
31	199	5.7	1277 21 AAB03149	Rat; synaptic staff
32	196.5	5.6	632 21 AAB01385	Neuron-associated
33	196.5	5.6	304 22 AAM93296	Human polypeptid
34	196.5	5.6	767 23 AAU04269	PDZ encoded domain
35	196.5	5.6	191 23 AAU97934	Human post-synapti
36	191	5.5	1535 23 AAB57623	Human post-synapti
37	189.5	5.4	188.5 22 AAB58035	Human polypeptid
38	188.5	5.4	469 22 AAM0870	PDZ domain-contain
39	186.5	5.3	40 22 AAY04736	Membrane-bound pro
40	185	5.3	344 22 AAB55834	
41	185	5.3	344 22 AAB57623	
42	185	5.3	344 22 AAB58035	
43	184.5	5.3	469 22 AAM0870	
44	184.5	5.3	590 20 AAY04736	
45	184.5	5.3	632 21 AAY6689	

XX (AURO-) AURORA BIOSCIENCES CORP.  
 PA (REGC ) UNITV CALIFORNIA.  
 XX  
 PI Mendlein JD, Sierralta J, Sun H, Tsunoda S, Zuker CS;  
 XX DR WPI; 1999-13222/11.  
 DR N-PSDB; AAX02832.  
 XX  
 PT Identifying modulators of signal transduction in cells - used to  
 PT treat signal transduction related disorders  
 PS Claim 9; Page 90-91; 96pp; English.  
 XX  
 CC This invention describes an insect, namely a fly, containing an amino acid mutation in a transducisome protein, InAd, that prevents functional binding of a signal transduction protein. A specific example of the mutation is described which occurs in the PDZ domain. The mutated protein can be used in a method for identifying modulators of signal transduction, cell surface receptors, ion channels or transducisomes, using cells that express the protein or heterologous protein containing a PDZ domain. The chemicals that modulate association of the protein with PDZ-binding proteins are useful for treating transducisome-related disorders. The transducisome protein can be expressed at high level in E. coli or other hosts, without requiring chemical synthesis or use of unnatural amino acid analogues.  
 CC  
 XX  
 SQ Sequence 674 AA;

Query Match Best Local Similarity 100.0%; Score 3490; DB 20; Length 674;  
 Matches 674; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC

QY 1 MVQFLGKQGTAGELIMVTLDTKGKSFGLCIVREVKSPNPKTGTGIFTGIVPDSPAH 60  
 Db 1 MVQFLGKQGTAGELIMVTLDTKGKSFGLCIVREVKSPNPKTGTGIFTGIVPDSPAH 60

QY 121 GYMQAKNKFNOEQTTNNASGGQGMQGQGQGMQRQGMNRQSMQRKNTFTASHRQHS 180  
 Db 121 GYMQAKNKFNOEQTTNNASGGQGMQGQGQGMQRQGMNRQSMQRKNTFTASHRQHS 180

QY 181 NYADEDDEDDTRDMTGRTEAYETDRASAGNCNLKQKDQKEDDEGYMAKINKR 240  
 Db 181 NYADEDDEDDTRDMTGRTEAYETDRASAGNCNLKQKDQKEDDEGYMAKINKR 240

QY 241 YNMMDKLRLREVORDASKPLGLLAGHKDROKMACFVASYDPNGALGSVDIKPGEIVEV 300  
 Db 241 YNMMDKLRLREVORDASKPLGLLAGHKDROKMACFVASYDPNGALGSVDIKPGEIVEV 300

QY 301 NGNVLKNRCHLNASAVFKNVDGDKLYMITSRRKPNDEGMCVPIKKFPMSDETFKIFDQ 360  
 Db 301 NGNVLKNRCHLNASAVFKNVDGDKLYMITSRRKPNDEGMCVPIKKFPMSDETFKIFDQ 360

QY 361 FPKARTVQVKRKEFGFGLGIMWYKHAEVGSCFISDLRESSNAELAGVKGDMLLAVNQDV 420  
 Db 361 FPKARTVQVKRKEFGFGLGIMWYKHAEVGSCFISDLRESSNAELAGVKGDMLLAVNQDV 420

QY 421 TLESWYDDATGLKRAEGVTMILTKSEEAIKAEEKKKEAKBEEKKEEAKFOEPATA 480  
 Db 421 TLESWYDDATGLKRAEGVTMILTKSEEAIKAEEKKKEAKBEEKKEEAKFOEPATA 480

QY 481 EIKPNKKLIELKVKPCKMCHRRLRQKOPCHDWLICNHPRLSGGOVAARKRLKIFDHICD 540  
 Db 481 EIKPNKKLIELKVKPCKMCHRRLRQKOPCHDWLICNHPRLSGGOVAARKRLKIFDHICD 540

QY 541 INGTPHVGSTMILTKVHOLHTTYKAVLTVFVRADPPELEKENFDLMMKAGKELGSL 600  
 Db 541 INGTPHVGSTMILTKVHOLHTTYKAVLTVFVRADPPELEKENFDLMMKAGKELGSL 600

QY 601 PNEIGCTIADIQYQPEIUSKLQRQDITRFNGALEGIPFQVQYALFKGANGKVSMEV 660  
 Db 601 PNEIGCTIADIQYQPEIUSKLQRQDITRFNGALEGIPFQVQYALFKGANGKVSMEV 660

QY 661 TRPKPTLTERAPKA 674  
 Db 661 TRPKPTLTERAPKA 674

RESULT 2  
 ABB5957  
 ID ABB5957 standard; Protein; 674 AA.

XX  
 AC ABB5957;  
 XX DT 26-MAR-2002 (first entry)  
 XX DE Drosophila melanogaster polypeptide SEQ ID NO 6663.  
 XX KW Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.

XX OS Drosophila melanogaster.  
 PN WO200171042-A2.  
 XX DD 27-SEP-2001.  
 XX PF 23-MAR-2001; 2001WO-US09231.  
 PR 23-MAR-2000; 2000US-19167P.  
 PR 11-JUL-2000; 2000US-0614150.  
 XX PA (PEKE ) PE CORP NY.  
 PI Venter JC, Adams M, Li PWD, Myers EW;  
 XX DR WPI; 2001-656860/75.  
 DR N-PSDB; ABL04060.

PT New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions.

PT Disclosure: SEQ ID NO 6663; 21pp + Sequence Listing; English.

CC The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (AB16176-AB130511), expressed DNA sequences (ABL0184-ABL16175) and the encoded proteins (ABL7737-ABL72072).

CC The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published-pct\\_sequences](http://ftp.wipo.int/pub/published-pct_sequences).

XX SQ Sequence 674 AA;

Query Match Best Local Similarity 95.3%; Score 3317; DB 22; Length 674;  
 Matches 654; Conservative 1; Mismatches 7; Indels 24; Gaps 3;

CC

QY 1 MVQFLGKQGTAGELIMVTLDTKGKSFGLCIVREVKSPNPKTGTGIFTGIVPDSPAH 60  
 Db 1 MVQFLGKQGTAGELIMVTLDTKGKSFGLCIVREVKSPNPKTGTGIFTGIVPDSPAH 60

QY 61 LGGRKVGDRLSLNGKDVVNSTEAVIDLIKAEFPKIELOFDKSDEQAKSDPRSN 120  
 Db 61 LGGRKVGDRLSLNGKDVVNSTEAVIDLIKAEFPKIELOFDKSDEQAKSDPRSN 120

QY 121 GYMQAKNKFNOEQTTNNASGGQGMQGQGQGMQRQGMNRQSMQRKNTFTASHRQHS 180

RA	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPheeson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Mosher A., Mount S.M., Moy N., Murphy B., Murphy D.M., Nelson D.L., Nelson D.R., Nelson K., Nixon K., Nussken D.R., Pacieb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Sjödin Klamroth I., Simpson M., Skupski M.P., Smith T., Spier E., Spadling A.C., Stapleton M., Strong R., Sun E., Swistkass R., Tector C., Turner R., Venter R., Wang A.H., Wang X., Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhou M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C., "The genome sequence of <i>Drosophila melanogaster</i> ,"; RT Science 287:2185-2195(2000).	Db	241 YNNMKDLRRIEVQDASKPLGLALGHKDQRKACPFVAGVDPNAGLSVDIKPGDETEV 300
RC	SEQUENCE FROM N.A.	Qy	301 NGNVLKNRCHLNASAVFKNVGDVKLVMITSRKFNEDCNCVPIKEPTASDTKFIDQ 360
RC	TISSUE=COMPOUND EYE;	Qy	361 FPKARTVVKRKEGFLGIVNIYGKHAEGSGIFPSDLRBGSNAELAGYVKGDMILLAVNDV 420
RT	Lindsay D.L., Zinn G.; "The genome of <i>Drosophila melanogaster</i> ,"; RT Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.	Db	361 FPKARTVVKRKEGFLGIVNIYGKHAEGSGIFPSDLRBGSNAELAGYVKGDMILLAVNDV 420
RL	SEQUENCE FROM N.A.	Qy	421 TLESNYDDATGLKRAASCYVMTLLTKESEELIKAERAAEKKKEEEAKKEEKKPQEATA 480
RN	[3]	Db	421 TLESNYDDATGLKRAASCYVMTLLTKESEELIKAERAAEKKKEEEAKKEEKKPQEATA 480
RP	TISSUE=COMPOUND EYE;	Qy	481 EIKPKNKLLIELKEVKEPKPMGCHRRLRQKPCDWL-----NPRLS-----GGVAA 528
RX	MEDLINE# 95127229; PubMed# 7826638;	Qy	589 KKAGKEGLSISLPNEIGCTIADLIGOPEIDSKLORGDIITKENGALELPEOCYAL 648
RC	Shieh B.H., Niemeyer B.; "A novel protein encoded by the inad gene regulates recovery of visual transduction in <i>Drosophila</i> ,"; RT Neuron 14:201-210(1995).	Db	481 EIKPKNKLLIELKEVKEPKPMG-----IVCGGKNHNTGCVITHVPPGVOAA 528
RN	[4]	Qy	529 DRRKIFDHICDINGPIHVGSMTLKHOLEHTVERAVTIVFVRADPELEKFNNDLM 588
RP	SEQUENCE FROM N.A.	Db	529 DKLKIFDHICDINGPIHVGSMTLKHOLEHTVERAVTIVFVRADPELEKFNNDLM 588
RC	TISSUE=COMPOUND EYE;	Qy	589 KKAGKEGLSISLPNEIGCTIADLIGOPEIDSKLORGDIITKENGALELPEOCYAL 648
RC	Shieh B.; "Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.	Db	649 FKGANGKVMSMEVTRPKTLTREAPKA 674
DR	EMBL; AE003458; AACF6915.1; .	Qy	649 FKGANGKVMSMEVTRPKTLTREAPKA 674
DR	HSSP; P31016; IBFE.	Db	649 FKGANGKVMSMEVTRPKTLTREAPKA 674
DR	FlyBase; FBgn0001263; inad.	Qy	649 FKGANGKVMSMEVTRPKTLTREAPKA 674
DR	InterPro; IPR001478; PDZ.	Db	649 FKGANGKVMSMEVTRPKTLTREAPKA 674
DR	Pfam; PF0059; PDZ; 5.	Qy	649 FKGANGKVMSMEVTRPKTLTREAPKA 674
DR	SMART; SM00228; PDZ; 5.	Db	649 FKGANGKVMSMEVTRPKTLTREAPKA 674
DR	PROSITE; PS50106; PDZ; 5.	Qy	649 FKGANGKVMSMEVTRPKTLTREAPKA 674
SQ	SEQUENCE 674 AA; 74332 MW; D4C24091D99EA7F3 CRC64;	Db	649 FKGANGKVMSMEVTRPKTLTREAPKA 674
<b>RESULT 2</b>			
RC	O9NBV3	ID	O9NBV3
RC	TISSUE=COMPOUND EYE;	AC	O9NBV3;
RL	Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.	DT	O1-OCT-2000 (TREMBLER, 15, Created)
RR	SEQUENCE FROM N.A.	DT	01-DEC-2001 (TREMBLER, 19, Last annotation update)
RC	TISSUE=COMPOUND EYE;	DE	INAD.
RC	Shieh B.; "Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.	GN	OS
DR	EMBL; AE003458; AACF6915.1; .	OC	Drosophila melanogaster (Fruit fly).
DR	HSSP; P31016; IBFE.	OC	Bukarrotta; Metzoco; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydioidea; Dirosophilidae; Drosophila.
DR	FlyBase; FBgn0001263; inad.	OC	NCBI_TaxId: 227;
DR	InterPro; IPR001478; PDZ.	DR	[1]
DR	Pfam; PF0059; PDZ; 5.	RP	SEQUENCE FROM N.A.
DR	SMART; SM00228; PDZ; 5.	RC	STRAIN=CANON-S;
DR	PROSITE; PS50106; PDZ; 5.	RA	Ashari M., Shieh B.; "The Inad locus in <i>Drosophila</i> ,";
SQ	SEQUENCE 674 AA; 74305 MW; 55B1C57B7A100F1D CRC64;	RT	"The Inad locus in <i>Drosophila</i> ,";
<b>RESULT 3</b>			
RC	O9NBV3	ID	O9NBV3
RC	TISSUE=COMPOUND EYE;	AC	O9NBV3;
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.	DT	O1-MAR-2000 (TREMBLER, 15, Created)
RR	SEQUENCE FROM N.A.	DT	01-DEC-2001 (TREMBLER, 19, Last annotation update)
RC	TISSUE=COMPOUND EYE;	DE	INAD.
DR	EMBL; AF25280; AACB1203.1; .	GN	OS
DR	HSSP; P31016; IBFE.	OC	Drosophila melanogaster (Fruit fly).
DR	FlyBase; FBgn0001263; inad.	OC	Bukarrotta; Metzoco; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydioidea; Dirosophilidae; Drosophila.
DR	InterPro; IPR001478; PDZ.	DR	NCBI_TaxId: 227;
DR	Pfam; PF0059; PDZ; 5.	DR	[1]
DR	SMART; SM00228; PDZ; 5.	DR	SEQUENCE FROM N.A.
DR	PROSITE; PS50106; PDZ; 5.	RC	STRAIN=CANON-S;
SQ	SEQUENCE 674 AA; 74305 MW; 55B1C57B7A100F1D CRC64;	RA	Ashari M., Shieh B.; "The Inad locus in <i>Drosophila</i> ,";
<b>RESULT 4</b>			
RC	O9NBV3	ID	O9NBV3
RC	TISSUE=COMPOUND EYE;	AC	O9NBV3;
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.	DT	O1-MAR-2000 (TREMBLER, 15, Created)
RR	SEQUENCE FROM N.A.	DT	01-DEC-2001 (TREMBLER, 19, Last annotation update)
RC	TISSUE=COMPOUND EYE;	DE	INAD.
DR	EMBL; AF25280; AACB1203.1; .	GN	OS
DR	HSSP; P31016; IBFE.	OC	Drosophila melanogaster (Fruit fly).
DR	FlyBase; FBgn0001263; inad.	OC	Bukarrotta; Metzoco; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydioidea; Dirosophilidae; Drosophila.
DR	InterPro; IPR001478; PDZ.	DR	NCBI_TaxId: 227;
DR	Pfam; PF0059; PDZ; 5.	DR	[1]
DR	SMART; SM00228; PDZ; 5.	DR	SEQUENCE FROM N.A.
DR	PROSITE; PS50106; PDZ; 5.	RC	STRAIN=CANON-S;
SQ	SEQUENCE 674 AA; 74305 MW; 55B1C57B7A100F1D CRC64;	RA	Ashari M., Shieh B.; "The Inad locus in <i>Drosophila</i> ,";
<b>RESULT 5</b>			
RC	O9NBV3	ID	O9NBV3
RC	TISSUE=COMPOUND EYE;	AC	O9NBV3;
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.	DT	O1-MAR-2000 (TREMBLER, 15, Created)
RR	SEQUENCE FROM N.A.	DT	01-DEC-2001 (TREMBLER, 19, Last annotation update)
RC	TISSUE=COMPOUND EYE;	DE	INAD.
DR	EMBL; AF25280; AACB1203.1; .	GN	OS
DR	HSSP; P31016; IBFE.	OC	Drosophila melanogaster (Fruit fly).
DR	FlyBase; FBgn0001263; inad.	OC	Bukarrotta; Metzoco; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydioidea; Dirosophilidae; Drosophila.
DR	InterPro; IPR001478; PDZ.	DR	NCBI_TaxId: 227;
DR	Pfam; PF0059; PDZ; 5.	DR	[1]
DR	SMART; SM00228; PDZ; 5.	DR	SEQUENCE FROM N.A.
DR	PROSITE; PS50106; PDZ; 5.	RC	STRAIN=CANON-S;
SQ	SEQUENCE 674 AA; 74305 MW; 55B1C57B7A100F1D CRC64;	RA	Ashari M., Shieh B.; "The Inad locus in <i>Drosophila</i> ,";
<b>RESULT 6</b>			
RC	O9NBV3	ID	O9NBV3
RC	TISSUE=COMPOUND EYE;	AC	O9NBV3;
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.	DT	O1-MAR-2000 (TREMBLER, 15, Created)
RR	SEQUENCE FROM N.A.	DT	01-DEC-2001 (TREMBLER, 19, Last annotation update)
RC	TISSUE=COMPOUND EYE;	DE	INAD.
DR	EMBL; AF25280; AACB1203.1; .	GN	OS
DR	HSSP; P31016; IBFE.	OC	Drosophila melanogaster (Fruit fly).
DR	FlyBase; FBgn0001263; inad.	OC	Bukarrotta; Metzoco; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydioidea; Dirosophilidae; Drosophila.
DR	InterPro; IPR001478; PDZ.	DR	NCBI_TaxId: 227;
DR	Pfam; PF0059; PDZ; 5.	DR	[1]
DR	SMART; SM00228; PDZ; 5.	DR	SEQUENCE FROM N.A.
DR	PROSITE; PS50106; PDZ; 5.	RC	STRAIN=CANON-S;
SQ	SEQUENCE 674 AA; 74305 MW; 55B1C57B7A100F1D CRC64;	RA	Ashari M., Shieh B.; "The Inad locus in <i>Drosophila</i> ,";
<b>RESULT 7</b>			
RC	O9NBV3	ID	O9NBV3
RC	TISSUE=COMPOUND EYE;	AC	O9NBV3;
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.	DT	O1-MAR-2000 (TREMBLER, 15, Created)
RR	SEQUENCE FROM N.A.	DT	01-DEC-2001 (TREMBLER, 19, Last annotation update)
RC	TISSUE=COMPOUND EYE;	DE	INAD.
DR	EMBL; AF25280; AACB1203.1; .	GN	OS
DR	HSSP; P31016; IBFE.	OC	Drosophila melanogaster (Fruit fly).
DR	FlyBase; FBgn0001263; inad.	OC	Bukarrotta; Metzoco; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydioidea; Dirosophilidae; Drosophila.
DR	InterPro; IPR001478; PDZ.	DR	NCBI_TaxId: 227;
DR	Pfam; PF0059; PDZ; 5.	DR	[1]
DR	SMART; SM00228; PDZ; 5.	DR	SEQUENCE FROM N.A.
DR	PROSITE; PS50106; PDZ; 5.	RC	STRAIN=CANON-S;
SQ	SEQUENCE 674 AA; 74305 MW; 55B1C57B7A100F1D CRC64;	RA	Ashari M., Shieh B.; "The Inad locus in <i>Drosophila</i> ,";
<b>RESULT 8</b>			
RC	O9NBV3	ID	O9NBV3
RC	TISSUE=COMPOUND EYE;	AC	O9NBV3;
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.	DT	O1-MAR-2000 (TREMBLER, 15, Created)
RR	SEQUENCE FROM N.A.	DT	01-DEC-2001 (TREMBLER, 19, Last annotation update)
RC	TISSUE=COMPOUND EYE;	DE	INAD.
DR	EMBL; AF25280; AACB1203.1; .	GN	OS
DR	HSSP; P31016; IBFE.	OC	Drosophila melanogaster (Fruit fly).
DR	FlyBase; FBgn0001263; inad.	OC	Bukarrotta; Metzoco; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydioidea; Dirosophilidae; Drosophila.
DR	InterPro; IPR001478; PDZ.	DR	NCBI_TaxId: 227;
DR	Pfam; PF0059; PDZ; 5.	DR	[1]
DR	SMART; SM00228; PDZ; 5.	DR	SEQUENCE FROM N.A.
DR	PROSITE; PS50106; PDZ; 5.	RC	STRAIN=CANON-S;
SQ	SEQUENCE 674 AA; 74305 MW; 55B1C57B7A100F1D CRC64;	RA	Ashari M., Shieh B.; "The Inad locus in <i>Drosophila</i> ,";
<b>RESULT 9</b>			
RC	O9NBV3	ID	O9NBV3
RC	TISSUE=COMPOUND EYE;	AC	O9NBV3;
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.	DT	O1-MAR-2000 (TREMBLER, 15, Created)
RR	SEQUENCE FROM N.A.	DT	01-DEC-2001 (TREMBLER, 19, Last annotation update)
RC	TISSUE=COMPOUND EYE;	DE	INAD.
DR	EMBL; AF25280; AACB1203.1; .	GN	OS
DR	HSSP; P31016; IBFE.	OC	Drosophila melanogaster (Fruit fly).
DR	FlyBase; FBgn0001263; inad.	OC	Bukarrotta; Metzoco; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydioidea; Dirosophilidae; Drosophila.
DR	InterPro; IPR001478; PDZ.	DR	NCBI_TaxId: 227;
DR	Pfam; PF0059; PDZ; 5.	DR	[1]
DR	SMART; SM00228; PDZ; 5.	DR	SEQUENCE FROM N.A.
DR	PROSITE; PS50106; PDZ; 5.	RC	STRAIN=CANON-S;
SQ	SEQUENCE 674 AA; 74305 MW; 55B1C57B7A100F1D CRC64;	RA	Ashari M., Shieh B.; "The Inad locus in <i>Drosophila</i> ,";
<b>RESULT 10</b>			
RC	O9NBV3	ID	O9NBV3
RC	TISSUE=COMPOUND EYE;	AC	O9NBV3;
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.	DT	O1-MAR-2000 (TREMBLER, 15, Created)
RR	SEQUENCE FROM N.A.	DT	01-DEC-2001 (TREMBLER, 19, Last annotation update)
RC	TISSUE=COMPOUND EYE;	DE	INAD.
DR	EMBL; AF25280; AACB1203.1; .	GN	OS
DR	HSSP; P31016; IBFE.	OC	Drosophila melanogaster (Fruit fly).
DR	FlyBase; FBgn0001263; inad.	OC	Bukarrotta; Metzoco; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydioidea; Dirosophilidae; Drosophila.
DR	InterPro; IPR001478; PDZ.	DR	NCBI_TaxId: 227;
DR	Pfam; PF0059; PDZ; 5.	DR	[1]
DR	SMART; SM00228; PDZ; 5.	DR	SEQUENCE FROM N.A.
DR	PROSITE; PS50106; PDZ; 5.	RC	STRAIN=CANON-S;
SQ	SEQUENCE 674 AA; 74305 MW; 55B1C57B7A100F1D CRC64;	RA	Ashari M., Shieh B.; "The Inad locus in <i>Drosophila</i> ,";
<b>RESULT 11</b>			
RC	O9NBV3	ID	O9NBV3
RC	TISSUE=COMPOUND EYE;	AC	O9NBV3;
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.	DT	O1-MAR-2000 (TREMBLER, 15, Created)
RR	SEQUENCE FROM N.A.	DT	01-DEC-2001 (TREMBLER, 19, Last annotation update)
RC	TISSUE=COMPOUND EYE;	DE	INAD.
DR	EMBL; AF25280; AACB1203.1; .	GN	OS
DR	HSSP; P31016; IBFE.	OC	Drosophila melanogaster (Fruit fly).
DR	FlyBase; FBgn0001263; inad.	OC	Bukarrotta; Metzoco; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydioidea; Dirosophilidae; Drosophila.
DR	InterPro; IPR001478; PDZ.	DR	NCBI_TaxId: 227;
DR	Pfam; PF0059; PDZ; 5.	DR	[1]
DR	SMART; SM00228; PDZ; 5.	DR	SEQUENCE FROM N.A.
DR	PROSITE; PS50106; PDZ; 5.	RC	STRAIN=CANON-S;
SQ	SEQUENCE 674 AA; 74305 MW; 55B1C57B7A100F1D CRC64;	RA	Ashari M., Shieh B.; "The Inad locus in <i>Drosophila</i> ,";